

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 23, 2002, 14:39:08 ; Search time 16.16 seconds

(without alignments)
1111.925 Million cell updates/sec

Title: US-09-811-118-1

Perfect score: 187
Sequence: 1 MVAATVAAAWLLMAAAQAQ.....VRLQITVALVKLLKREDL 187

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR_71.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 13 | 7.0 | 167 | 2 | T14262 glutathione peroxi |
| 2 | 11 | 5.9 | 169 | 2 | S75885 glutathione peroxi |
| 3 | 10 | 5.3 | 160 | 2 | F87463 glutathione peroxi |
| 4 | 10 | 5.3 | 163 | 2 | T23936 hypothetical prote |
| 5 | 10 | 5.3 | 236 | 2 | T06462 glutathione peroxi |
| 6 | 9 | 4.8 | 116 | 2 | S56693 glutathione peroxi |
| 7 | 9 | 4.8 | 134 | 2 | S68899 glutathione peroxi |
| 8 | 9 | 4.8 | 163 | 2 | T21418 hypothetical prote |
| 9 | 9 | 4.8 | 167 | 1 | S33618 glutathione peroxi |
| 10 | 9 | 4.8 | 169 | 1 | S20501 probable glutathio |
| 11 | 9 | 4.8 | 169 | 2 | T04207 phospholipid-hydro |
| 12 | 9 | 4.8 | 170 | 1 | JN0608 phospholipid-hydro |
| 13 | 9 | 4.8 | 170 | 1 | JC4332 phospholipid-hydro |
| 14 | 9 | 4.8 | 171 | 2 | JC5619 phospholipid-hydro |
| 15 | 9 | 4.8 | 173 | 2 | T48097 glutathione peroxi |
| 16 | 9 | 4.8 | 180 | 2 | T12633 glutathione peroxi |
| 17 | 9 | 4.8 | 192 | 2 | C96660 protein P2K1.16 l |
| 18 | 9 | 4.8 | 206 | 2 | A84865 glutathione peroxi |
| 19 | 9 | 4.8 | 230 | 2 | T06309 glutathione peroxi |
| 20 | 9 | 4.8 | 236 | 2 | A86644 glutathione peroxi |
| 21 | 9 | 4.8 | 242 | 1 | S71250 probable glutathio |
| 22 | 8 | 4.3 | 169 | 2 | D84722 glutathione peroxi |
| 23 | 8 | 4.3 | 171 | 2 | A84924 probable glutathio |
| 24 | 8 | 4.3 | 193 | 2 | T16662 hypothetical prote |
| 25 | 8 | 4.3 | 449 | 2 | C82688 tryptophan synthas |
| 26 | 8 | 4.3 | 508 | 2 | E81875 threonine dehydrat |
| 27 | 8 | 4.3 | 508 | 2 | E81875 threonine dehydrat |
| 28 | 8 | 4.3 | 769 | 2 | S35458 SNF2 protein homol |
| 29 | 8 | 4.3 | 1531 | 2 | T42218 slit-1 protein hom |

| | | | | | |
|----|---|-----|-----|---|---------------------------|
| 30 | 7 | 3.7 | 96 | 2 | S65794 glutathione peroxi |
| 31 | 7 | 3.7 | 122 | 2 | S05317 glutathione peroxi |
| 32 | 7 | 3.7 | 122 | 2 | H83110 50S ribosomal prot |
| 33 | 7 | 3.7 | 126 | 2 | D83475 hypothetical prote |
| 34 | 7 | 3.7 | 155 | 2 | S56258 hypothetical prote |
| 35 | 7 | 3.7 | 158 | 2 | T43376 glutathione peroxi |
| 36 | 7 | 3.7 | 158 | 2 | D89905 glutathione peroxi |
| 37 | 7 | 3.7 | 160 | 2 | F83541 probable glutathio |
| 38 | 7 | 3.7 | 161 | 2 | H83292 probable glutathio |
| 39 | 7 | 3.7 | 162 | 2 | S46121 probable glutathio |
| 40 | 7 | 3.7 | 162 | 2 | T09638 probable glutathio |
| 41 | 7 | 3.7 | 163 | 1 | S48499 glutathione peroxi |
| 42 | 7 | 3.7 | 167 | 2 | T44271 glutathione peroxi |
| 43 | 7 | 3.7 | 174 | 2 | B83673 hypothetical prote |
| 44 | 7 | 3.7 | 183 | 1 | ORECBE vitamin B12 transp |
| 45 | 7 | 3.7 | 183 | 2 | A98931 vitamin B12 transp |

ALIGNMENTS

RESULT 1
T14262
glutathione peroxidase (EC 1.11.1.9) - common sunflower
C:Species: Helianthus annuus (common sunflower)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C:Accession: T14262
R.Roeckel-Drevet, P.; Gagne, G.; Tourville de Labrouhe, D.; Dufaire, J.P.; Nicolas, Physiol. Plantarum 103, 385-394, 1998
A:Title: Molecular characterization, organ distribution and stress-mediated induction
A:Reference number: 217562
A:Accession: T14262
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-167 <ROE>
A:Cross-References: EMBL:Y14429
C:Genetics:
A:Gene: GPxha-1
C:Function:
A:Description: catalyzes reduction of hydroperoxides by glutathione, thus protecting
C:Superfamily: glutathione peroxidase
C:Keywords: oxidoreductase

Query Match 7.0%; Score 13; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.8e-05;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 82 LAEPNQGQGP 94
Db 66 LAEPNQGQGP 78

RESULT 2
S75885
glutathione peroxidase homolog sir1171 - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein sir1171
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S75885
R.Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocys*
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S75885
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-169 <KAN>
A:Cross-References: EMBL:D90913; GB:AB001339; NID:g1653348; PIDN:BA18344.1; PID:g165
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C:Superfamily: glutathione peroxidase

Query Match 5.9%; Score 11; DB 2; Length 169;
 Best Local Similarity 100.0%; Pred. No. 0.002;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 84 FPCNOFGOEP 94
 |||||||||
 Db 67 FPCNOFGOEP 77

RESULT 3

F87463
 glutathione peroxidase [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
 C:Accession: F87463
 R:Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Taub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A:Title: Complete Genome Sequence of *Caulobacter crescentus*.
 A:Reference number: A87249; MIMD:21173698; PMID:11259647
 A:Accession: F87463

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-160 <STO>
 A:Cross-references: GB:AE005673; NID:gl3423148; PIDN:AAK23706.1; GSPDB:GN00148
 C:Genetics:
 A:Gene: CCI1730
 C:Superfamily: glutathione peroxidase

Query Match 5.3%; Score 10; DB 2; Length 160;
 Best Local Similarity 100.0%; Pred. No. 0.02;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFCNOFG 90
 |||||||||
 Db 60 VLAFCNOFG 69

RESULT 4
 T23936
 hypothetical protein R05H10.5 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*
 C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T23936
 R:McMurray, A.
 submitted to the EMBL Data Library, November 1996

A:Reference number: Z19820
 A:Accession: T23936
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-163 <MIL>
 A:Cross-references: EMBL:Z83119; PIDN:CAB05581.1; GSPDB:GN00020; CESP:R05H10.5
 A:Experimental source: clone R05H10
 C:Genetics:
 A:Gene: CESP:R05H10.5
 A:Map position: 2
 A:Introns: 23/2; 52/2
 C:Superfamily: glutathione peroxidase

Query Match 5.3%; Score 10; DB 2; Length 163;
 Best Local Similarity 100.0%; Pred. No. 0.021;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFCNOFG 90
 |||||||||
 Db 60 VLAFCNOFG 69

RESULT 5

T06462
 glutathione peroxidase (EC 1.11.1.9) precursor - garden pea

N:Alternate names: phospholipid glutathione peroxidase
 C:Species: *Pisum sativum* (garden pea)
 C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
 C:Accession: T06462
 R:Muilleaux, P.M.; Karpinski, S.; Jimenez, A.; Cleary, S.P.; Robinson, C.; Creissen,
 Plant J. 13, 375-379, 1998
 A:Title: Identification of cDNAs encoding plastid-targeted glutathione peroxidase.
 A:Reference number: Z15696; MIMD:98345965
 A:Accession: T06462

A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-236 <MUD>
 A:Cross-references: EMBL:AJ000508; NID:g2632108; PIDN:CAA04142.1; PID:g2632109
 A:Experimental source: cv. Blüte
 C:Genetics:
 A:Map position: 1
 A:Genome: nuclear
 C:Superfamily: glutathione peroxidase
 C:Keywords: chloroplast; oxidoreductase; selenocysteine

Query Match 5.3%; Score 10; DB 2; Length 236;
 Best Local Similarity 100.0%; Pred. No. 0.029;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFCNOFG 90
 |||||||||
 Db 135 VLAFCNOFG 144

RESULT 6

S56693
 glutathione peroxidase (EC 1.11.1.9) - wild oat (fragment)

C:Species: *Avena fatua* (wild oat)
 C:Date: 10-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 11-Jun-1999
 C:Accession: S56693
 R:Johnson, R.R.; Cranston, H.J.; Chaverra, M.E.; Dyer, W.E.
 Plant Mol. Biol. 28, 113-122, 1995
 A:Title: Characterization of cDNA clones for differentially expressed genes in embryo
 A:Reference number: S56690; MIMD:95306780
 A:Accession: S56693

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-116 <JON>
 A:Cross-references: EMBL:U20000; NID:g726477; PIDN:AAV6742.1; PID:g726478
 A:Experimental source: clone AFN3
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995
 C:Superfamily: glutathione peroxidase
 C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNOFG 90
 |||||||||
 Db 15 LAFCNOFG 23

RESULT 7

S68899

glutathione peroxidase (EC 1.11.1.9) - fluke (*Schistosoma mansoni*) (fragments)

C:Species: *Schistosoma mansoni*
 C:Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 12-Dec-1997
 C:Accession: S68899
 R:Majorino, M.; Roche, C.; Kiess, M.; Koenig, K.; Gawlik, D.; Mattes, M.; Naldini, E.
 Eur. J. Biochem. 238, 838-844, 1996
 A:Title: A selenium-containing phospholipid-hydroperoxide glutathione peroxidase in *S*

A:Reference number: S68899; MUID:96300252
A:Accession: S68899
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11;12-25;26-28;29-67;68-82;83-134 <MAT>
C:Superfamily: glutathione peroxidase
C:Keywords: oxidoreductase; selenium; selenocysteine

Query Match 4.8%; Score 9; DB 2; Length 134;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNCFG 90
|||||
DB 48 LAFCNCFG 56

RESULT 8

T21418
hypothetical protein F26E4.12 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 21-Jan-2000
C:Accession: T21418
R:Lightning, J.
Submitted to the EMBL Data Library, October 1996
A:Reference number: Z19419
A:Accession: T21418
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-163 <WIL>
A:Cross-references: EMBL:Z81070; PIDN:CA803004.1; GSPDB:GN00019; CESP:F26E4.12
A:Experimental source: clone F26E4
C:Genetics:
A:Gene: CESP:F26E4.12
A:Map position: 1
A:Introns: 23/2; 52/2
C:Superfamily: glutathione peroxidase

Query Match 4.8%; Score 9; DB 2; Length 163;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 VLAFPCNOF 89
|||||
DB 60 VLAFPCNOF 68

RESULT 9

S33618
glutathione peroxidase (EC 1.11.1.9) - sweet orange
N:Alternate names: salt-associated protein csaa
C:Species: Citrus sinensis (sweet orange)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S33618; S36373
R:Holland, D.; Ben-Hayim, G.; Faltin, Z.; Camolin, L.; Strosberg, A.D.; Eshdat, Y.
Plant Mol. Biol. 21, 923-927, 1993
A:Title: Molecular characterization of salt-stress-associated protein in citrus: protein
A:Reference number: S33618; MUID:93222490
A:Accession: S33618
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-167 <HOL>
A:Cross-references: EMBL:X66377
A:Note: part of this sequence was confirmed by protein sequencing
R:Holland, D.
Submitted to the EMBL Data Library, May 1992
A:Reference number: S36373
A:Accession: S36373
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-52, 0', 54-167 <HOZ>

A:Cross-references: EMBL:X66377; NID:g296357; PIDN:CAA47018.1; PID:g296358
C:Genetics:
A:Gene: csaa
C:Superfamily: glutathione peroxidase
C:Keywords: oxidoreductase; selenocysteine
F:41/Modified site: selenocysteine #status predicted

Query Match 4.8%; Score 9; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNCFG 90
|||||
DB 66 LAFCNCFG 74

RESULT 10

S20501
probable glutathione peroxidase (EC 1.11.1.9) - wood tobacco
C:Species: Nicotiana glauca (wood tobacco)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: S20501
R:Ciriql, M.C.; Jamet, E.; Parmentier, Y.; Marbach, J.; Durr, A.; Fleck, J.
Plant Mol. Biol. 18, 623-627, 1992
A:Title: Isolation and characterization of a plant cDNA showing homology to animal gl
A:Reference number: S20501; MUID:92163033
A:Accession: S20501
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-169 <CRI>
A:Cross-references: EMBL:X60219; NID:g19738; PIDN:CAA42780.1; PID:g19739
C:Superfamily: glutathione peroxidase
C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFCNCFG 90
|||||
DB 68 LAFCNCFG 76

RESULT 11

T04207
phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - Arabidopsis thaliana
N:Alternate names: protein TSC23.30
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 03-Nov-2000
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
Submitted to the Protein Sequence Database, March 1999
A:Reference number: T25261
A:Accession: T04207
A:Molecule type: DNA
A:Residues: 1-169 <BEV>
A:Cross-references: EMBL:AL049500
A:Experimental source: cultivar Columbia; BAC clone TSC23
R:Bilodeau, P.
Submitted to the EMBL Data Library, October 1997
A:Reference number: T25116
A:Accession: T52116
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-169 <BIT>
A:Cross-references: EMBL:AF030132; PIDN:AAC09173.1
C:Genetics:
A:Map position: 4
A:Introns: 16/3; 42/2; 63/1; 102/3; 158/3
A:Note: TSC23.30
C:Superfamily: glutathione peroxidase

C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90
|||||
DB 67 LAFPCNOFG 75

RESULT 12

phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - pig
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JN0608; A53395; A54649
R:Sunde, R.A.; Dyer, J.A.; Moran, T.V.; Evenson, J.K.; Sugimoto, M.
Biochem. Biophys. Res. Commun. 193, 905-911, 1993
A>Title: Phospholipid hydroperoxide glutathione peroxidase: full-length pig blastocyst
A:Reference number: JN0608; MUID:93312346
A:Accession: JN0608
A:Molecule type: mRNA
A:Residues: 1-170 <SUN>
A:Cross-references: GB:U12743; NID:9294224; PIDN:AAA31099.1; PID:9294226
A:Experimental source: blastocyst
R:Brigelius-Flohe, R.; Annann, K.D.; Bloeker, H.; Gross, G.; Kiess, M.; Kloeppel, K.D.;
J. Biol. Chem. 269, 7342-7348, 1994
A>Title: Phospholipid-hydroperoxide glutathione peroxidase. Genomic DNA, cDNA, and deduc
A:Reference number: A53395; MUID:94171752
A:Accession: A53395
A>Status: Preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-45, 'S', '47-170

A:Cross-references: GB:X76008; NID:9473358; PIDN:CAA53595.1; PID:92654294; GB:X76009; NT
R:Schuckelt, R.; Brigelius-Flohe, R.; Maiorino, M.; Roveri, A.; Reumens, J.; Strassburg
Free Radic. Res. Commun. 14, 343-361, 1991
A>Title: Phospholipid hydroperoxide glutathione peroxidase is a selenoenzyme distinct fr
A:Reference number: A54649; MUID:92137773
A:Accession: A54649
A>Status: Preliminary
A:Molecule type: mRNA; protein
A:Residues: 13-45, 47-170 <SCH>
A:Cross-references: GB:S80257; NID:9244650; PIDN:ABD21327.1; PID:9244651
A:Experimental source: heart
A>Note: sequence extracted from NCBI backbone (NCBIN:80257, NCBI:P:80258)
C:Superfamily: glutathione peroxidase
C:Keywords: oxidoreductase; selenocysteine
F:46/Modified site: selenocysteine #status predicted

Query Match 4.8%; Score 9; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90
|||||
DB 71 LAFPCNOFG 79

RESULT 13

phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: J04332
R:Imai, H.; Sumi, D.; Hanamoto, A.; Arai, M.; Sugiyama, A.; Chiba, N.; Kuchino, Y.; Nak
J. Biochem. 118, 1061-1067, 1995
A>Title: Molecular cloning and functional expression of a cDNA for rat phospholipid hyd
A:Reference number: J04332; MUID:96318522
A:Accession: J04332
A:Molecule type: mRNA

A:Residues: 1-170 <IMA>

A:Cross-references: EMBL:X82679; NID:91041644; PIDN:CAA57996.1; PID:91041645
A:Experimental source: brain
C:Comment: This enzyme is a unique enzyme in glutathione peroxidase and is a selenopr
es. It defenses against oxidative destruction of biomembranes.
C:Genetics:
A:Introns: 45/3
C:Superfamily: glutathione peroxidase
C:Keywords: brain; oxidoreductase; phospholipid; selenocysteine
F:46/Modified site: selenocysteine #status experimental

Query Match 4.8%; Score 9; DB 1; Length 170;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90
|||||
DB 71 LAFPCNOFG 79

RESULT 14

phospholipid-hydroperoxide glutathione peroxidase (EC 1.11.1.12) - spinach
N:Alternate names: peroxidation-inhibiting protein
C:Species: Spinacia oleracea (spinach)
C>Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 20-Jun-2000
C:Accession: J05619
R:Sugimoto, M.; Futui, S.; Suzuki, Y.
Biosci. Biotechnol. Biochem. 61, 1379-1381, 1997
A>Title: Molecular cloning and characterization of a cDNA encoding putative phosphol
A:Reference number: J05619; MUID:97446534
A:Accession: J05619
A:Molecule type: mRNA
A:Residues: 1-171 <SUC>
A:Cross-references: DDBJ:D63425; NID:92392020; PIDN:BA22194.1; PID:92392021
C:Comment: This enzyme catalyzes the reduction of hydroperoxides of phospholipids act
C:Genetics:
A:Gene: phgpx
C:Superfamily: glutathione peroxidase
C:Keywords: oxidoreductase

Query Match 4.8%; Score 9; DB 2; Length 171;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 82 LAFPCNOFG 90
|||||
DB 69 LAFPCNOFG 77

RESULT 15

glutathione peroxidase-like protein - Arabidopsis thaliana
N:Alternate names: protein T20010.180
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 19-May-2000
C:Accession: T48097
R:Obermayer, B.; Ottenwelder, B.; Duchemin, D.; Zeitler, K.; Newes, H.W.; Rudd, S.;
submitted to the Protein Sequence Database, April 2000
A:Reference number: Z24484
A:Accession: T48097
A>Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-173 <OBE>
A:Cross-references: EMBL:AL163816
A:Experimental source: cultivar Columbia; BAC clone T20010
C:Genetics:
A:Map position: 3
A:Introns: 20/3; 46/2; 67/1; 106/3; 162/3
A>Note: T20010.180
C:Superfamily: glutathione peroxidase

Query Match 4.8%; Score 9; DB 2; Length 173;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 VLAFCNDF 89
|||||||
Db 70 VLAFCNDF 78

Search completed: August 23, 2002, 14:41:16
Job time: 128 sec

